

NetworkKIN is an integrated framework for modeling kinase-substrate interactions and aid in the design of inhibitor-based follow-up perturbation experiments. An interactive web interface allows investigation of predicted kinase-substrate interactions from human and major eukaryotic model organisms.

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Set your organism
Human

Paste sequences (FASTA format) or protein names (one per line) below
In case you have more than 100 sequences, please consider using the [high throughput workflow](#).

Example: [#1](#), [#2](#), [#3](#)

The web service allows a user to submit protein sequence, name, or id.

Select Phosphosites

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Let's start with example sequences

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Set your organism

Human



Paste sequences (FASTA format) or protein names (one per line) below

Example:[#1](#), [#2](#), [#3](#)

In case you have more than 100 sequences, please consider using the [high throughput workflow](#).

```
>O00151
MTTQQIDLQGGPGWGFRLVGGKDFEQPLAISRVTPGSKAALANLCIGDVITAIDGENTSNMTHLEAQNRIGCTDNLTLTVARSEHKVWSPLVTEEGKRHPYKMNLASEPQEV
HIGSAHNRSAMPFTASPASSTTARVITNQYNNPAGLYSSENISNFNNALESKTAASGVEANSRPLDHAQPPSSLVIDKESEVYKMLQEKQELNEPPKQSTSFLVLQEILESEEK
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>O00418
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HRYNAVTEWLDDEVLIKMASQPFGRGAMRECFRTKKLSNFLHAQQWKGASNYVAKRYIEPVDRDVYFEDVRLQMEAKLWGEENRHKPPKQVDIMQMCIIEKDRPGKPLFH
LEHYIEGKYIKYNSNSGFVRDDNIRLTPQAFSHFTFERSGHLIVVDIQGVGDLYTDPQIHTETGTDFGDGNLGVRGMALFFYSHACNRICESMGLAPFDLSPRERDAVNQNTKLL
QSAKTILRGTEEKCGSPQVRTLSGSRPPLRLPLENSGDENMSDVTFDLSPSSPSATPHSQKLDHLHWPVFSLDNMA SRDHDHLDNHRESENSGDSGYPSEKRGELDDPEPRE
HGHSYSNRKYESDEDSLGSGRVCVEKWNLLNSSRLHLPRASAVALEVQRLNALDLEKKIGKSILGKVHLAMVRYHEGGRFCEKGEEDQESAVFHLEHAANLGELEAIVGLGLM
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>P55196
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WNKDDREGRFVLKNENDAIPPKAQSNQPEKQEKEGVQNFKRTL SKKEKKEKKREKEALRQASDKDDRPFQGEDVENSRLAAEVYKDM PETSFTRTISNPEVVMKRRRQQKLE
KRMQEFRSSDGRPDSSGGLRIYADSLKPNIPYKTILLSTTDPADFAVAEAELEKYGLEKENPKDYCIARVMLPPGAQHSD EKGAKIILDDDECPLQIFREWPSDKGILVFQLKRRPPD
HIPKTKKHLEGKTPKGKERADGSGYGSTLPPEKLPYLVELSPDGS DSRDKPKLYRLQLSVTEVGTEKLDDNSIQLFGPGIQPHHCDLTNMDGVVTVTPRSM DAETYVEGQRISET
TMLQSGMKVQFGASHVFKFVDP SQDHALAKRSVDGGLMVKGPRHKPGIVQETTFDLGGDIHSGTALPTSKSTTRLDSDRVSSASSTAERG MVKPMIRVEQQPDYRRQESRTQD
ASGP ELILPASIEFRESEDSFLSAIINYTN SSTVHFKLSPTYVLYMACRYVLSNQYRPDISPTERTHKVI AVVNKMVSMMEGVIQKQKNIAGALAFWMANASELLNFIKQDRDLSRIT
LDAQDVL AHLVQMAFKYLVHCLQSELNNYMPAFLDDPEENSLQRPKIDDLHTLTGAMSLLRRCRVNAALTIQLFSQLFHF INMWLFNRLVTDPD SGLCSHYWGAIIRQQLGHI/
```

Select Phosphosites

Click

NetworkKIN suggests proteins based on sequence homology



The submitted sequences mapped to multiple targets in ENSEMBL (e-value <1e-40, identity >90%)
Please specify the right one.

Next

Q9z266

☒ PDPK2 ⓘ

☐ SNAPAP ⓘ

☐ PDPK1 ⓘ

Q9Z2H5

☒ EPB41L1 ⓘ

O00418

☒ EEF2K ⓘ

P55196

☒ MLLT4 ⓘ

Q9Z2Q6


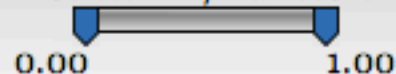
☒ SEPT5 ⓘ

O00151

☒ PDLIM1 ⓘ

Next

Click
after confirming that the suggested proteins are right ones

Select min/max score 

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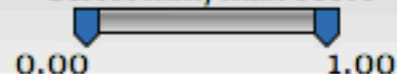


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		SKAQKSPQKI AKKFKSAICR VTLLDASEYE CEVEKHGRGQ VLFDLVCEHL NLLEKDYFGL TYCDADSQKN WLDPSKEIKK 160 EN
		QIRSSPWNEA FTVKFYPPDP AQLTEDITRY YLCLQLRADI ITGRLPCSFV THALLGSYAV QALGDDYDAE EHVGNVYSEL 240
		RFAPNQIREL EERIMELHKT YRGMTPEAE IHFLENAKKL SMYGVDLHHA KDSEGIDIML GVCANGLLIY RDRLRINRFA 320
		WPKILKISYK RSNFYIKIRP GEYEQFESTI GFKLPNHRSA KRLWKVCIEH HTFFRLVSPE PPPKGFLVMG SKFRYSGRTQ 400
		AQTRQASALI DRPAPFFERS SSKRYTMSRS LDGAEFSPRA SVSENHDAGP DGDKREDDAE SGGRRSEAE GEVRTPTKIK 480
		ELKPEQETTP RHKQEFLDKP EDVLLKHQAS INELKRTLKE PNSKLIHRDR DWDRERRRLPS SPASPSPKGT PEKASERAGL 560
		REGSEKVKP PRPRAPESDT GDEDQDQERD AVFLKDNHLA IERKCSSITV SSTSSLEAEV DFTVIGDYHG GAFEDFSRSL 640
		PELDRDKSDS ETEGLVFARD LKGPSSQDE SGGLEDSPDR GACSTPEMPQ FESVKAETMT VSSLAIRKKI EPEAMLQSRV 720
		SAADSTQVDG GTPMVKDFMT TPPCITTETI STTMENSLKS GKGAAMIPG PQTVATEIRS LSPPIGKDV LSTSTTHVT KTVKGGFSET RIEKRIITG DEDVDQDQAL ALAIKEAKLQ HPDMLVTKAV VYRETDPSP EREDKKPQES 880
2	000418 ENSP00000263026	MADEDLIFRL EGVDGGQSPR AGHDGSDSDG SDDEEGYFI ITDDGSM NVSSNKKYK SUTKSENYK SSSNKKYK 160
		FKEAWKHAIQ KAKHMPDPWA EFHLEDIATE RATRHRYNV TGEWLDDEV LKMASQPFGR GAMRECFRTK KLINFLHAQQ 160
		WKGASNYVAK RYIEPVDRDV YFEDVRLQME AKLWGEENR HKPPKQVDN OMCIIEKDR PGKPLEHLEH YIEGKYIKYN 240
		SNSGFVRDDN IRLTPQAFSH FTFERSGHQL IVVDIQGVG YLTPQIHG ITDGLVNL QVGMALGEI YSENQITES 320
		MGLAPFDLSP RERDAVNQNT KLLQSAKTIL RGTEEKCGSP QVRTLSGSRP PLLRPLSENS GDENMSDVTF DSLPSSPSSA 400
		TPHSQKLDHL HWPVFSDDL N MASRDHDHLD NHRESENSGD SGYPSEKRGE LDDPEPREHG SSSSSSSSS SGR 480
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		LGELEAIVGL GLMYSQLP HH ILADVSLKET EENKTKGFDY LLKAAEAGDR QSMILVARAF DSGQNLSPDR QDWLEALHW 640
		YNTALEMTDC DEGGEYDGMQ DEPRYMMLAR EAEMLF TGGY GLEKDPQSRG DLYTQAAEAA MEAMKGR LAN QYYQKAEAW 720
		AQMEE 800
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		VARSEHKVWS PLVTEEGKRH PYKMNLASEP QEVLHIGSAH NRSAMPFTAS PASSTTARVI TNQYNNPAGL YSSENISNFN 160
		NALESKTAAS GVEANSRPLD HAQPPSSLVI DKESEVYKML QEKQELNEPP KQSTSFLVLQ EILESEEKGD PNKPSGFRSV 240
		KAPVTKVAAS IGNAQKLPMC DKCGTGIVGV FVKLRDRHRH PECYVCTDCG TNLKQKGHFF VEDQIYCEKH ARERVTPPEG 320
		YEVVTVFPKS QSQSQSQSQ 400
4	Q9Z2Q6 ENSP00000328190	QYVGFA TLPN QVHRKSVKKG FDF TLMVAGE SGLGKSTLVH SLFLTDLKYD RKLLSAEERI NQTV EILKHT VDIEEKGVKL 80
		KLTI VDT PGF GDAVN NSECW KPITDYVDQO FEQYFRDESG LNRKNIQDNR VHCCLYFISP FGHGLRPVDV GFMKALHEKV 160
		NIVPLIAKAD CLVPSEIRKL KDRIREEIDK FGIHVYQFPE CDSDEDEDFK QQDRELKESA PFAVIGSNTV VEAQGQVRVG 240
		RLYPWGIVEV ENQAHCDFVK LRNMLIRTHM HDLKDV TCDV HYENYRAHCI QQMTSKLTQD SRMESPIPI PLPTPDAETE 320
		KLIRMKDEEL RRMQEMLOKM KQMQDQ 400
5	Q9Z266 ENSP00000371763	MAAAGSAAVS GAGTPVAGPT GRDLFAEGLL EFLRPAVQQL DSHVHAVRES QVELREQIDN LATELCRINE DQKVALDLDP 80
		YVKKLLNARR RVVLVNNILQ NAQERLRLRN HSVAKETARR RAMLD SGVYP PGSPSKQAMA RTTSQLYDAV PIQSSVVLCS 160
		CPSPSMVRSQ TEPGSSPGIP SGVSRQGSTM DGTTAEARPS TNPLQOHPAQ LPPQPRKKRP EDFKFGKILG EGSFSTVLA 240
		RELATSREYA IKILEKRHI KENKVPYVTR ERDVMSRLDH PFFVKLYFTF QDDEKLYFGL SYAKNGELLK YIRKIGSFDE 320
		TCTRFYTAEI VSALEYLHGK GIIHRDLKPE NILLNEDMHI QITDFGTAKV LSPESKQARA NSFVGTAQYV SPELLTEKSA 400
		CKSSDLWALG CIIYQLVAGL PPFRAGNEYL IFQKIIKLEY HFPEKFFPKA RDLVEKLLVL DATKRLGCEE MEGYGPLKAH 480
		PFFETITWEN LHQQTTPKLT AYLPA MSED EDCYGN YDNL LSQFGFMQVS SSSSSHSLST VETSLPQSRG SNIEQYI HDL 560
		DTNSFELDLQ FSEDEKRLLL EKQAGGNPWH QFVENNLILK MGPVDKRKGL FARRRQ LLLT EGP HLYYVDP VNKVLKGEIP 640
		WSQELRPEAK NFKTFFVHTP NRTYYLMDPS GNAHKWCRKI QEVWRQYQS NPDAAVQ 720

Click

You can choose phosphorylation sites, other the server takes all S,T,Y sites as candidates

Select min/max score


☐ High throughput experiments

☐ Low throughput experiments

☐ Load sites from file:

 N...

i


1	Q9Z2H5 ENSP00000337168	MTTETGPDSE VKKAQEETPO QPEAAAAVTT PVTPAGHSHP ETNSNEKHLT QQDTRPAEQS LDMDDKDYSE ADGLSERTTP 806	PE
		SKAQKSPQKI AKKFKSAICR VTLLDASEYE CEVEKHGRGQ VLFDLVCEHL NLEKDYFGL TYCDADSQKN WLDPSKEIKK 160	EN
		QIRSSPWNFA FTVKFYPPDP AQLTEDITRY YLCLQLRADI ITGRLPCSFV THALLGSYAV QAELGDYDAE EHVGNVYSEL 240	
		RFAPNQTRER EERIMELHKT YRGMTPEAE IHFLENAKKL SMYGVDLHHA KDSEGIDIML GVCANGLLIY RDRLRINRFA 320	
		WPKILKISYK RSNFYIKIRP GEYEQFESTI GFKLPNHRSA KRLWKVCIEH HTFFRLVSPE PPPKGFLVMG SKFRYSGRTO 400	
		AQTRQASALI DRPAPFFERS SSKRYTMSRS LDGAEFSPRA SVSENHDAGP DGDKREDDAE SGGRRSEAE EGVRTPTKIK 480	
		ELKPEQETTP RHKQEFLDKP EDVLLKHQAS INELKRTLKE PNSKLIHRDR DWDRERRRLPS SPASPSPKG TPEKASERAGL 560	
		REGSEKVKP PRPRAPESDT GDEDQDQERD AVFLKDNHLA IERKCSSITV SSTSSLEAEV DFTVIGDYHG GAFEDFSRSL 640	
		PELDRDKSDS ETEGLVFARD LKGPSSQEDE SGGLEDSPDR GACSTPEMPQ FESVKAETMT VSSLAIRKKI EPEAMLQSRV 720	
		SAADSTQVDG GTPMVKDFMT TPPCITTETI STTMENSLKS GKGAAMIPG PQTVATEIRS LSPIIGKDV LSTSTTTHVT KTVKGGPST 880	
		MADEDLIFRL EGVDG SSGSPANSFH 80	
		FKEAWKHAIQ KAKHM KLSNFLHAQQ 160	
		WKGASNYVAK RYIEP YIEGKYIKYN 240	
		SNSGFVRDDN IRLTP SHACNRICES 320	
		MGLAPFDLSP RERDA DSLPSSPSA 400	
		TPHSQKLDHL HWPVF DEDSLGSSGR 480	
		VCVEKWNLLN SSR LH AVFHLEHAAN 560	
		LGELEAIVGL GLMYS CQDWLEALHW 640	
		YNTALEMTDC DEGGE QYYQKAEAW 720	
		AQMEE 800	
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		NALESKTAAS GVEANSRPLD HAQPPSSLVI DKESEVYKML QEKQELNEPP KQSTSFLVLQ EILESEEKGD PNKPSGFRSV 240	
		KAPVTKVAAS IGNAQKLPMC DKCGTGIVGV FVKLRDRHRH PECYVCTDCG TNLKQKGHFF VEDQIYCEKH AREVTPPIG 320	
		YEVVTVFPKS QSQSQSQSQ 400	
4	Q9Z2Q6 ENSP00000328190	QYVGFAATLPN QVHRKSVKKG FDFTLMVAGE SGLGKSTLVH SLFLTDLYKD RKLLSAEERI NQTVETILKHT VDIEEKGVKL 80	
		KLTIVDTPGF GDAVNNSECW KPITDYVDQQ FEQYFRDESG LNRKNIQDNR VHCCLYFISP FGHGLRPVDV GFMKALHEKV 160	
		NIVPLIAKAD CLVPSEIRKL KDRIREIDK FGIHVYQFPE CDSDEDEDFK QODRELKESA PFAVIGSNTV VEAQGQVRVG 240	
		RLYPWGIVEV ENQAHCDFVK LRNMLIRTHM HDLKDVTCDV HYENYRAHCI QQMTSKLTQD SRMESPIPI LPLTPDAETE 320	
		KLIRMKDEEL RRMQEMLOKM KQQMQDQ 400	
5	Q9Z266 ENSP00000371763	MAAAGSAAVS GAGTPVAGPT GRDLFAEGLL EFLRPAVQQ L DSHVHAVRES QVELREQIDN LATELCRINE DQKVALDLDP 80	
		YVKKLLNARR RVVLVNNILQ NAQERLRLN HSVAKETARR RAMLD SGVYP PGSPSKQAMA RTTSQLYDAV PIQSSVVLCS 160	
		CPSPSMVRSQ TEPGSSPGIP SGVSRQGSTM DGTTAEARPS TNPLQOHPAQ LPPQPRKKRP EDFKFGKILG EGSFSTVVLA 240	
		RELATSREYA IKILEKRHI KENKVPYVTR ERDVM SRLDH PFFVKLYFTF QDDEKLYFGL SYAKNGELLK YIRKIGSFDE 320	
		TCTRFYTAEI VSALEYLHGK GIIHRDLKPE NILLNEDMHI QITDFGTAKV LSPE SKQARA NSFVGTAQYV SPELLTEKSA 400	
		CKSSDLWALG CIIYQLVAGL PPFRAGNEY L IFQKIIKLEY HFPEKFFPKA RDLVEKLLVL DATKRLGCEE MEGYGPLKAH 480	
		PFFETITWEN LHQQTPPKLT AYLPA SEDD EDCYGN YDNL LSQFGFMQVS SSSSSSHSLST VETSLPQ RSG SNIEQYI HDL 560	
		DTNSFELDLO FSEDEKRLLL EKQAGGNPWH QFVENNLILK MGPVDKRKGL FARRRQLLT EGP HLYYVDP VNKVLKGEIP 640	
		WSQELRPEAK NFKTFFVHTP NRTYYLMDPS GNAHKWCRKI QEVWRQYQ S NPDAAVQ 720	




The page at kinomexplorer.info says:

No sites for prediction selected

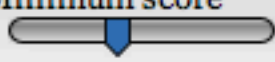
Should the prediction run on all sites?

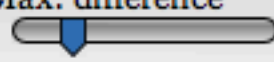
Click

Results

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Minimum score  2.00

Max. difference  1.00

☒ KIN ☐ 14-3-3 ☐ BRCT
☒ PTB ☒ SH2 ☐ WW

Max. # of Predictions

Real time filter for results ☒



000151				
000418				
S18	Kinase	MAPK13	2.0509	VDGGSPPRAGH
S74	Kinase	MAPK13	2.0509	YSSSGSPANSF
T254	Kinase	MAPK13	2.0168	DNIRLTTPQAFS
S359	Kinase	MAPK13	2.0168	EEKCGSPQVRT
S366	Kinase	p70S6Kb	2.8915	QVRTLSGSRPP
		p70S6K	2.6063	QVRTLSGSRPP
S396	Kinase	MAPK13	2.0509	DSLSPSSSAT
T401	Kinase	MAPK13	2.0509	SPSSATPHSQK
S464	Kinase	p70S6Kb	2.5262	HGHSYSNRKYE
		p70S6K	2.3401	HGHSYSNRKYE
P55196				
Y1235	PTB	FRS2	2.0402	NQWPNYEEKPH
Q9Z2H5				
Q9Z2Q6				
Q9Z266				
T20	Kinase	PKCiota	2.0760	PVAGPTGRDLF
S112	Kinase	PKCiota	2.0760	RRLNHSAKET
T117	Kinase	PKCiota	2.2127	SAKETARRRA
S301	Kinase	PKCiota	2.3665	LYFGLSYAKNG
T367	Kinase	PKCiota	2.2127	ITDFGTAKVLS

Kinases that are predicted to phosphorylate the site

Residues that are predicted to be phosphorylated

Exercise

Q. Using NetworKIN, Find top 3 kinases that are predicted to phosphorylate S39 position in human N-RAS protein.

Protein sequence of human N-RAS

```
>sp|P01111|RASN_HUMAN GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1
MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAG
QEEYSAMRDQYMRTGEGFLCVFAINNSKSFADINLYREQIKRVKDSDDVPMVLVGNNKCDL
PTRTVDTKQAHELAKSYGIPFIETSAKTRQGVEDAFYTLVREIRQYRMKKLNSSDDGTQG
CMGLPCVVM
```

NetworKIN web site

<http://kinomexplorer.info/>

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